

SEQUENCE LISTING

<110> Dale Umetsu  
Rosemarie DeKruyff  
Jennifer McIntire  
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH  
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344

<151> 2001-06-29

<150> 10/188,012

<151> 2002-07-01

<160> 58

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 305

<212> PRT

<213> M. musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-1 BALB/c allele

<400> 1

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Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
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 20      25      30
Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
 35      40      45
Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
 50      55      60
Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
 65      70      75      80
Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
 85      90      95
Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
 100     105     110
Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys
 115     120     125
Pro Glu Ile Pro Thr Arg Pro Pro Thr Arg Pro Thr Thr Thr Arg Pro
 130     135     140
Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val
 145     150     155     160
Pro Thr Ser Ile Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
 165     170     175
Thr Trp Thr His Lys Pro Glu Pro Thr Thr Phe Cys Pro His Glu Thr
 180     185     190
Thr Ala Glu Val Thr Gly Ile Pro Ser His Thr Pro Thr Asp Trp Asn
 195     200     205
Gly Thr Val Thr Ser Ser Gly Asp Thr Trp Ser Asn His Thr Glu Ala
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Ile Pro Pro Gly Lys Pro Gln Lys Asn Pro Thr Lys Gly Phe Tyr Val

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[illegible]

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<211> 918
<212> DNA
<213> Mus musculus
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aacttaaggg	ggcatatttt	agaaggagat	gtgtccttga	cgatagagaa	ctctgtttgag	300	
agtgacagtg	gtctgtattg	ttgtcgagtg	gagattcctg	gatggtttaa	tgatcagaaa	360	
gtgacctttt	cattgcaagt	taaaccagag	attcccacac	gtcctccaac	aagaccaca	420	
actacaagcg	ccacagctac	aggaagaccc	acgactattt	caacaagatc	cacacatgta	480	
ccaacactca	tcagagtctc	tacctccact	ctccaacatc	ctacacacac	atggactcac	540	
aaaccagaac	ccactacatt	ttgtccccat	gagacaacag	ctgaggtgac	aggaatccca	600	
tcccatactc	ctacagactg	gaatggcact	gtgacatcct	caggagatac	ctggagtaat	660	
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tacatactta	tgaaaaggaa	gtcagcatct	ctaagcgtgg	ttgccttcgg	tgtctctaag	840	
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<210> 3
<211> 282
<212> PRT
<213> Mus musculus
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<220>
<221> VARIANT
<222> (1)...(282)
<223> TIM-1, C.D2 ES-HBA and DBA/2J allele
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Gly	Ala	Val	Asp	Ser	Tyr	Val	Glu	Val	Lys	Gly	Val	Val	Gly	His	Pro	
			20					25					30			
Val	Thr	Leu	Pro	Cys	Thr	Tyr	Ser	Thr	Tyr	Arg	Gly	Ile	Thr	Thr	Thr	
		35					40					45				
Cys	Trp	Gly	Arg	Gly	Gln	Cys	Pro	Ser	Ser	Ala	Cys	Gln	Asn	Thr	Leu	
	50					55					60					
Ile	Trp	Thr	Asn	Gly	His	Arg	Val	Thr	Tyr	Gln	Lys	Ser	Ser	Arg	Tyr	
65					70					75					80	
Asn	Leu	Lys	Gly	His	Ile	Ser	Glu	Gly	Asp	Val	Ser	Leu	Thr	Ile	Glu	
				85					90					95		
Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile	
			100					105					110			
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys	
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## Seq1ist\_12\_20\_06.txt

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Pro Glu Ile Pro Thr Arg Pro Pro Arg Arg Pro Thr Thr Thr Arg Pro
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Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val
145 150 155 160
Pro Thr Ser Thr Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
165 170 175
Thr Trp Thr His Lys Pro Asp Trp Asn Gly Thr Val Thr Ser Gly
180 185 190
Asp Thr Trp Ser Asn His Thr Glu Ala Ile Pro Pro Gly Lys Pro Gln
195 200 205
Lys Asn Pro Thr Lys Gly Phe Tyr Val Gly Ile Cys Ile Ala Ala Leu
210 215 220
Leu Leu Leu Leu Val Ser Thr Val Ala Ile Thr Arg Tyr Ile Leu
225 230 235 240
Met Lys Arg Lys Ser Ala Ser Leu Ser Val Val Ala Phe Arg Val Ser
245 250 255
Lys Ile Glu Ala Leu Gln Asn Ala Ala Val Val His Ser Arg Ala Glu
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Asp Asn Ile Tyr Ile Val Glu Asp Arg Pro
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<210> 4  
 <211> 849  
 <212> DNA  
 <213> Mus musculus

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caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcgggtac 240
aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300
agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360
gtgacctttt cattgcaagt taaaccagag attcccacac gtcctccaag aagacccaca 420
actacaaggc ccacagctac aggaagaccc acgactattt caacaagatc cacacatgta 480
ccaacatcaa ccagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
aaaccagatc ggaatggcac tgtgacatcc tcaggagata cctggagtaa tcacactgaa 600
gcaatccctc caggggaagcc gcagaaaaaac cctactaagg gcttctatgt tggcatctgc 660
atcgagccc tgctgtact gctccttgtg agcaccgtgg ctatcaccag gtacatactt 720
atgaaaagga agtcagcatc tctaagcgtg gttgccttcc gtgtctctaa gattgaagct 780
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849

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<210> 5  
 <211> 305  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(305)  
 <223> TIM-2 BALB/c allele

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<400> 5
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Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
35 40 45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
50 55 60

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## Seq1ist\_12\_20\_06.txt

Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg  
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 Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile  
 85 90 95  
 Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu  
 100 105 110  
 Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro  
 115 120 125  
 Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro  
 130 135 140  
 Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val  
 145 150 155 160  
 Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro  
 165 170 175  
 Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu  
 180 185 190  
 Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser  
 195 200 205  
 Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro  
 210 215 220  
 Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala  
 225 230 235 240  
 Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val  
 245 250 255  
 Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile  
 260 265 270  
 Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys  
 275 280 285  
 Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu  
 290 295 300  
 Ser  
 305

<210> 6  
 <211> 958  
 <212> DNA  
 <213> Mus musculus

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 tcaccctgtc acacttccat gtattttattc gacacacctt ggtggaatcg ttcctatgtg 180  
 ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240  
 atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300  
 aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtcctt attgctgtgt 360  
 agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420  
 ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480  
 atccacacat gtaccaacat caaccagagt ctctacctt acttctcaa caccagcaca 540  
 cacagagacc tacaaaccag aggccactac attttatcca gatcagacta cagctgaggt 600  
 gacagaaacc ttaccctcta ctctgcaga ctggcataac actgtgacat cctcagatga 660  
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 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780  
 ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgttgctt 840  
 ccctatctct aagattggag cttcccccac aaaagtggc gaacggacca gatgtgaaga 900  
 ccaggtctac attattgaag acactcctta ccctgaagaa gagtcctagt gcctctac 958

<210> 7  
 <211> 305  
 <212> PRT  
 <213> Mus musculus

<220>

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(305)

&lt;223&gt; TIM-2, C.D2 ES-HBA and DBA/2J allele

&lt;400&gt; 7

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Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
 1      5      10      15
Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
 20      25      30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35      40      45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50      55      60
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65      70      75      80
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85      90      95
Glu Asn Thr Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
100      105      110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115      120      125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130      135      140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145      150      155      160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165      170      175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180      185      190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195      200      205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210      215      220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225      230      235      240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245      250      255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
260      265      270
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
275      280      285
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
290      295      300
Ser
305

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&lt;210&gt; 8

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 8

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tcaccctgtc acacttccat gtatttattc gacacacctt ggtggaatcg ttcttatgtg 180
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atatacggtc acacatcaga ggaacagtcg ataccagcta aagggggaata ttccagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtccct attgctgtgt 360
agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga ccacaacta tttcaacaag 480
atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
cacagagacc tacaaccag aggccactac attttatcca gatcagacta cagctgaggt 600

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seqlist\_12\_20\_06.txt

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 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780  
 gggtatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct tcgttgccct 840  
 ccctatctct aagattggag cttcccccaa aaaagtgggc gaacggacca gatgtgaaga 900  
 ccaggtctac attattgaag acactcctta ccccgaagaa gaggcctagt gcctctac 958

<210> 9  
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 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(281)  
 <223> TIM-3 BALB/c allele

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 Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu  
 35 40 45  
 Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr  
 50 55 60  
 Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser  
 65 70 75 80  
 Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu  
 85 90 95  
 Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg  
 100 105 110  
 Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu  
 115 120 125  
 Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp  
 130 135 140  
 Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser  
 145 150 155 160  
 Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile  
 165 170 175  
 Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr  
 180 185 190  
 Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu  
 195 200 205  
 Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys  
 210 215 220  
 Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly  
 225 230 235 240  
 Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr  
 245 250 255  
 Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr  
 260 265 270  
 Cys Tyr Val Asn Ser Gln Gln Pro Ser  
 275 280

<210> 10  
 <211> 2725  
 <212> DNA  
 <213> Mus musculus

<400> 10  
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Seq1ist\_12\_20\_06.txt

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<210> 11  
 <211> 281  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(281)  
 <223> TIM-3, C.D2 ES-HBA and DBA/2J allele

<400> 11  
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 Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys  
 20 25 30  
 Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu  
 35 40 45

## Seq1ist\_12\_20\_06.txt

Val	Pro	Met	Cys	Trp	Gly	Lys	Gly	Phe	Cys	Pro	Trp	Ser	Gln	Cys	Thr
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65					70					75					80
Ser	Arg	Tyr	Gln	Leu	Lys	Gly	Asp	Leu	Asn	Lys	Gly	Asp	Val	Ser	Leu
			85						90					95	
Ile	Ile	Lys	Asn	Val	Thr	Leu	Asp	Asp	His	Gly	Thr	Tyr	Cys	Cys	Arg
			100					105					110		
Ile	Gln	Phe	Pro	Gly	Leu	Met	Asn	Asp	Lys	Lys	Leu	Glu	Leu	Lys	Leu
		115					120					125			
Asp	Ile	Lys	Ala	Ala	Lys	Val	Thr	Pro	Ala	Gln	Thr	Ala	His	Gly	Asp
		130				135					140				
Ser	Thr	Thr	Ala	Ser	Pro	Arg	Thr	Leu	Thr	Thr	Glu	Arg	Asn	Gly	Ser
					150					155					160
Glu	Thr	Gln	Thr	Leu	Val	Thr	Leu	His	Asn	Asn	Asn	Gly	Thr	Lys	Ile
				165					170					175	
Ser	Thr	Trp	Ala	Asp	Glu	Ile	Lys	Asp	Ser	Gly	Glu	Thr	Ile	Arg	Thr
			180					185					190		
Ala	Ile	His	Ile	Gly	Val	Gly	Val	Ser	Ala	Gly	Leu	Thr	Leu	Ala	Leu
		195					200					205			
Ile	Ile	Gly	Val	Leu	Ile	Leu	Lys	Trp	Tyr	Ser	Cys	Lys	Lys	Lys	Lys
		210				215					220				
Leu	Ser	Ser	Leu	Ser	Leu	Ile	Thr	Leu	Ala	Asn	Leu	Pro	Pro	Gly	Gly
					230					235					240
Leu	Ala	Asn	Ala	Gly	Ala	Val	Arg	Ile	Arg	Ser	Glu	Glu	Asn	Ile	Tyr
				245					250					255	
Thr	Ile	Glu	Glu	Asn	Val	Tyr	Glu	Val	Glu	Asn	Ser	Asn	Glu	Tyr	Tyr
				260				265					270		
Cys	Tyr	Val	Asn	Ser	Gln	Gln	Pro	Ser							
		275					280								

<210> 12  
 <211> 862  
 <212> DNA  
 <213> Mus musculus

<400> 12  
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 actactactt gcaaggatcat tggaaaatgc ttatgtgttt gaggttggta agaatgccta 120  
 tctgccctgc agttacactc tatctacacc tggggcactt gtgcctatgt gctggggcaa 180  
 gggattctgt ccttggtcac agtgtaccaa cgagttgctc agaactgatg aaagaaatgt 240  
 gacatatcag aaatccagca gataccagct aaaggcgat ctcaacaaag gagacgtgtc 300  
 tctgatacata aagaatgtga ctctggatga ccatgggacc tactgctgca ggatacagtt 360  
 ccctgggtctt atgaatgata aaaaattaga actgaaatta gacatcaaag cagccaaggt 420  
 cactccagct cagactgccc atggggactc tactacagct tctccaagaa ccctaaccac 480  
 ggagagaaat gggtcagaga cacagacact ggtgaccctc cataataaca atggaacaaa 540  
 aatttccaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca 600  
 cattggagtg ggagtctctg ctgggttgac cctggcactt atcattgggtg tcttaatcct 660  
 taaatgggtat tcctgtaaga aaaagaagtt atcgagtttg agccttatta cactggccaa 720  
 cttgcctcca ggagggttgg caaatgcagg agcagtcagg attcgctctg aggaaaatat 780  
 ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagtact actgctacgt 840  
 caacagccag cagccatcct ga 862

<210> 13  
 <211> 345  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(345)  
 <223> TIM-4, BALB/c allele



## Seqlist\_12\_20\_06.txt

&lt;400&gt; 13

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1      5      10      15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
 20      25      30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
 35      40      45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
 50      55      60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
 65      70      75      80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
 85      90      95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100      105      110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115      120      125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130      135      140
Thr Thr Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145      150      155      160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
165      170      175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180      185      190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195      200      205
Ser Ala Ile Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210      215      220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225      230      235      240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245      250      255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260      265      270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275      280      285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290      295      300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305      310      315      320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325      330      335
Asp Asp Glu Asp Gly Ile Phe Thr Leu
340      345

```

&lt;210&gt; 14

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 14

```

atgtccaagg ggcttctcct cctctggctg gtgacggagc tctggtggct ttatctgaca 60
ccagctgcct cagaggatac aataataggg tttttgggcc agccggtgac ttgacctgt 120
cattacctct cgtggtccca gagccgcaac agtatgtgct ggggcaaagg ttcattgtcc 180
aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
tcaacaaaat atacactttt ggggaagggtc cagtttggtg aagtgtcctt gaccatctca 300
aacaccaatc gaggtgacag tggggtgtac tgctgccgta tagaggtgcc tggctggttc 360
aatgatgtca agaagaatgt gcgcttgagag ctgaggagag ccacaacaac caaaaaacca 420
acaacaacca cccggccaac caccaccctt tatgtaacca ccaccacccc agagctgctt 480
ccaacaacag tcatgaccac atctgttctt ccaaccacca caccaccca gacactagcc 540

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Seqlist\_12\_20\_06.txt

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accactgcct tcagtacagc agtgaccacg tgccccctcaa caacacctgg ctcctttctca 600
caagaaacca caaaaggggtc cgccatcact acagaatcag aaactctgcc tgcattccaat 660
cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gcccacaggc 720
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
ttgatcattg cctgctgtgt gggatttgtg ctaatgggtg tattgtttct ggcgtttctc 900
cttcgagggg aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
ttcactctct ga                                     1032

```

<210> 15

<211> 345

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(345)

<223> C.D2 ES-HBA and DBA/2J allele

<400> 15

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp
1      5      10      15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20      25      30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35      40      45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50      55      60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65      70      75      80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85      90      95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100      105      110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115      120      125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130      135      140
Thr Thr Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145      150      155      160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
165      170      175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180      185      190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195      200      205
Ser Ala Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210      215      220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225      230      235      240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245      250      255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260      265      270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275      280      285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290      295      300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305      310      315      320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325      330      335

```

Asp Asp Glu Asp Gly Ile Phe Thr Leu  
340 345

<210> 16  
<211> 1032  
<212> DNA  
<213> Mus musculus

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<400> 16
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ccagctgcct cagaggatac aataataggg tttttgggcc agccgggtgac tttgccttgt 120
cattacctct cgtgggtccca gagccgcaac agtatgtgct ggggcaaagg ttcattgtccc 180
aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
tcaacaaaat atacactttt ggggaagggtc cagtttgggtg aagtgtcctt gaccatctca 300
aacaccaatc gaggtgacag tgggggtgtac tgctgccgta tagagggtgcc tggctgggttc 360
aatgatgtca agaagaatgt gcgcttgagg ctgaggagag ccacaacaac caaaaaacca 420
acaacaacca cccggccaac caccacccct tatgtaacca ccaccacccc agagctgctt 480
ccaacaacag tcatgaccac atctgtttctt ccaaccacca caccacccca gacactagcc 540
accactgcct tcagtcacag agtgaccacg tgcccctcaa caacacctgg ctctttctca 600
caagaaacca caaaagggtc cgccttctact acagaatcag aaactctgcc tgcattccaat 660
cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gcccacaggc 720
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
acaagtgagt ctttgacgaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
ttgatcattg cctgctgtgt gggatttgtg ctaatgggtg tattgtttct ggcgtttctc 900
cttcgagggg aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
ttcactctct ga 1032
```

<210> 17  
<211> 359  
<212> PRT  
<213> H. sapiens

<220>  
<221> VARIANT  
<222> (1)...(360)  
<223> TIM-1 allele 1

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<400> 17
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1      5      10      15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20      25      30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35      40      45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50      55      60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65      70      75      80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85      90      95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100      105      110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115      120      125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130      135      140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr
145      150      155      160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr
165      170      175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
```

## Seqlist\_12\_20\_06.txt

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      180
Thr Thr Thr Ser Val Pro Val Thr Thr Val Ser Thr Phe Val Pro
      185
      190
      195
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
      200
      205
      210
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
      215
      220
      225
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
      230
      235
      240
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
      245
      250
      255
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
      260
      265
      270
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala
      275
      280
      285
      290
Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
      295
      300
      305
Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
      310
      315
      320
Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
      325
      330
      335
      340
Asn Ser Leu Tyr Ala Thr Asp
      345
      350
      355

```

<210> 18  
 <211> 1080  
 <212> DNA  
 <213> H. sapiens

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<400> 18
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tctgtaaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgcca ctacagtggg 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
ggcgatatatt gttgccgtgt tgagcacctg gggtgggtca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caagggtcacg actactccaa ttgtcacaac tgttccaacc 420
gtcacgactg ttggaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaac 600
acaacggctc ctacctttgt tcctccaatg cttttgcccc ggcagaacca tgaaccagta 660
gccattcac catcttcacc tcagccagca gaaaccacc ctacgacact gcagggagca 720
ataaggagag aacccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gactctgtat ttctgtcttg 900
gtgcttcttg ctcttttggg tgatcatcatt gccaaaagt atttcttcaa aaaggagggt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtccttatgc cacggactaa 1080

```

<210> 19  
 <211> 359  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(359)  
 <223> TIM-1, allele 2

<400> 19  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp

## SeqList\_12\_20\_06.txt

1	5	10	15
Ser Val Ala Gly	Ser Val Lys Val Gly	Gly Glu Ala Gly	Pro Ser Val
20	25	30	35
Thr Leu Pro Cys	His Tyr Ser Gly	Ala Val Thr Ser	Met Cys Trp Asn
40	45	50	55
Arg Gly Ser Cys	Ser Leu Phe Thr	Cys Gln Asn Gly	Ile Val Trp Thr
60	65	70	75
Asn Gly Thr His	Val Thr Tyr Arg	Lys Asp Thr Arg	Tyr Lys Leu Leu
80	85	90	95
Gly Asp Leu Ser	Arg Arg Asp Val	Ser Leu Thr Ile	Glu Asn Thr Ala
100	105	110	115
Val Ser Asp Ser	Gly Val Tyr Cys	Cys Arg Val Glu	His Arg Gly Trp
120	125	130	135
Phe Asn Asp Met	Lys Ile Thr Val	Ser Leu Glu Ile	Val Pro Pro Lys
140	145	150	155
Val Thr Thr Thr	Pro Ile Val Thr	Thr Thr Val Pro	Thr Val Thr Thr
160	165	170	175
Arg Thr Ser Thr	Thr Val Pro Thr	Thr Thr Thr Val	Pro Thr Thr Thr
180	185	190	195
Val Pro Thr Thr	Met Ser Ile Pro	Thr Thr Thr Val	Pro Thr Thr Thr
200	205	210	215
Met Thr Val Ser	Thr Thr Thr Ser	Val Pro Thr Thr	Thr Ser Ile Pro
220	225	230	235
Thr Thr Thr Ser	Val Pro Val Thr	Ala Val Ser Thr	Phe Val Pro
240	245	250	255
Pro Met Pro Leu	Pro Arg Gln Asn	His Glu Pro Val	Ala Thr Ser Pro
260	265	270	275
Ser Ser Pro Gln	Pro Ala Glu Thr	His Pro Thr Thr	Leu Gln Gly Ala
280	285	290	295
Ile Arg Arg Glu	Pro Thr Ser Ser	Pro Leu Tyr Ser	Tyr Thr Thr Asp
300	305	310	315
Gly Asn Asp Thr	Val Thr Glu Ser	Ser Asp Gly Leu	Trp Asn Asn Asn
320	325	330	335
Gln Thr Gln Leu	Phe Leu Glu His	Ser Leu Leu Thr	Ala Asn Thr Thr
340	345	350	355
Lys Gly Ile Tyr	Ala Gly Val Cys	Ile Ser Val Leu	Val Leu Leu Ala
360	365	370	375
Leu Leu Gly Val	Ile Ile Ala Lys	Lys Tyr Phe Phe	Lys Lys Glu Val
380	385	390	395
Gln Gln Leu Ser	Val Ser Phe Ser	Ser Leu Gln Ile	Lys Ala Leu Gln
400	405	410	415
Asn Ala Val Glu	Lys Glu Val Gln	Ala Glu Asp Asn	Ile Tyr Ile Glu
420	425	430	435
Asn Ser Leu Tyr	Ala Thr Asp		

&lt;210&gt; 20

&lt;211&gt; 1080

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;400&gt; 20

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attgtctgga	ccaatggaac	ccacgtcacc	tatcggaagg	acacacgcta	taagctattg	240
ggggaccttt	caagaaggga	tgtctctttg	accatagaaa	atacagctgt	gtctgacagt	300
ggcgtatatt	gttgccgtgt	tgagcaccgt	gggtgggtca	atgacatgaa	aatcaccgta	360
tcattggaga	ttgtgccacc	caaggtcacg	actactccaa	ttgtcacaac	tggtccaacc	420
gtcacgactg	ttcgaacgag	caccactgtt	ccaacgacaa	cgactgttcc	aacgacaact	480
gttccaacaa	caatgagcat	tccaacgaca	acgactgttc	cgacgacaat	gactgtttca	540
acgacaacga	gcgttccaac	gacaacgagc	attccaacaa	caacaagtgt	tccagtgaca	600

seqlist\_12\_20\_06.txt

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acagcgggtct ctacctttgt tcctccaatg cctttgccc ggcagaacca tgaaccagta 660
gccacttcac catcttcacc tcagccagca gaaaccacc ctacgacact gcagggagca 720
ataaggagag aacccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggagggt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

```

<210> 21  
 <211> 365  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(365)  
 <223> TIM-1, allele 3

<400> 21

Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp
1			5				10						15		
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val
		20					25					30			
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn
		35				40						45			
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr
	50				55					60					
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu
	65				70				75					80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala
			85					90					95		
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp
		100					105					110			
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
		115				120					125				
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130				135					140					
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr
	145				150				155					160	
Thr	Val	Pro	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	
			165				170					175			
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro
		180				185						190			
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ala
	195				200						205				
Val	Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu
	210				215					220					
Pro	Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro
	225				230			235						240	
Thr	Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu
		245						250					255		
Tyr	Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp
		260			265							270			
Gly	Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu
	275				280						285				
Leu	Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser
	290				295					300					
Val	Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr
	305				310				315						320
Phe	Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu
			325					330						335	

## Seq1ist\_12\_20\_06.txt

Gln Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu  
 340 345 350  
 Asp Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp  
 355 360 365

<210> 22  
 <211> 1098  
 <212> DNA  
 <213> H. sapiens

<400> 22  
 atgcatcctc aagtgggtcat ctttaagcctc atcctacatc tggcagattc tgtagctggt 60  
 tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgcca ctacagtgga 120  
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180  
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360  
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420  
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480  
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540  
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600  
 acaagtgttc cagtgaacac arcggtctct acctttgttc ctccaatgcc ttgtcccagg 660  
 cagaacctatg aaccagtagc cacttcacca tcttcacctc agccagcaga aacccaccct 720  
 acgacactgc agggagcaat aaggagagaa cccaccagct caccattgta ctcttacaca 780  
 acagatggga atgacaccgt gacagagtct tcagatggcc tttggaataa caatcaaact 840  
 caactgttcc tagaacatag tctactgacg gccaatacca cttaaaggaat ctatgctgga 900  
 gtctgtatatt ctgtcttggg gcttcttggc cttttgggtg tcatcattgc caaaaagtat 960  
 ttcttcaaaa aggaggttca acaactaagt gtttcattta gcagccttca aattaaagct 1020  
 ttgcaaaatg cagttgaaaa ggaagtccaa gcagaagaca atatctacat tgagaatagt 1080  
 ctttatgccca cggactaa 1098

<210> 23  
 <211> 359  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(359)  
 <223> TIM-1, allele 4

<400> 23  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp  
 1 5 10 15  
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val  
 20 25 30  
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn  
 35 40 45  
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr  
 50 55 60  
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu  
 65 70 75 80  
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala  
 85 90 95  
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp  
 100 105 110  
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys  
 115 120 125  
 Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val  
 130 135 140  
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr  
 145 150 155 160

## Seq1ist\_12\_20\_06.txt

Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr  
 165 170 175  
 Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro  
 180 185 190  
 Thr Thr Thr Ser Val Pro Val Thr Thr Ser Val Ser Thr Phe Val Pro  
 195 200 205  
 Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro  
 210 215 220  
 Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Thr  
 225 230 235 240  
 Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp  
 245 250 255  
 Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Ser Asn Asn  
 260 265 270  
 Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr  
 275 280 285  
 Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala  
 290 295 300  
 Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val  
 305 310 315 320  
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln  
 325 330 335  
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu  
 340 345 350  
 Asn Ser Leu Tyr Ala Thr Asp  
 355

<210> 24  
 <211> 1079  
 <212> DNA  
 <213> H. sapiens

<400> 24  
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60  
 tctgttaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgcca ctacagtgga 120  
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180  
 attgtcttga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360  
 tcattggaga ttgtgccacc caagggtcacg actactccaa ttgtcacaac tgttccaacc 420  
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480  
 gttccaacaa caatgagcat tccaacgaca acggactgtt ccgacgacaa tgactgtttc 540  
 aacgacaacg agcgttccaa cgacaacgag cattccaaca acaacaagtg ttccagtgtg 600  
 aacatgtctc tacctttgtt cctccaatgc ctttggccag gcagaaccat gaaccagtag 660  
 ccacttcacc atcttcacct cagccagcag aaacccaccc tacgacactg cagggagcaa 720  
 taaggagaga acccaccagc tcaccattgt actcttacac aacagatggg aatgacaccg 780  
 tgacagagtc ttcagatggc ctttggarta acaatcaaac tcaactgttc ctagaacata 840  
 gtctactgac ggccaatacc actaaaggaa tctatgtctg agtctgtatt tctgtcttgg 900  
 tgcttcttgc tcttttgggt gtcatcattg ccaaaaagta tttcttcaaa aaggagggtc 960  
 aacaactaag tgtttcattt agcagccttc aaattaaagc tttgcaaaat gcagttgaaa 1020  
 aggaagtcca agcagaagac aatatctaca ttgagaatag tctttatgcc acggactaa 1079

<210> 25  
 <211> 364  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(364)  
 <223> TIM-1 allele 5



## Seqlist\_12\_20\_06.txt

&lt;400&gt; 25

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Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1      5      10      15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20      25      30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35      40      45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50      55      60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65      70      75      80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85      90      95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100     105     110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115     120     125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130     135     140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Met Thr Thr
145     150     155     160
Thr Val Pro Thr Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165     170     175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180     185     190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val
195     200     205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210     215     220
Val Ala Thr Ser Pro Ser Pro Gln Pro Ala Glu Thr His Pro Thr
225     230     235     240
Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
245     250     255
Ser Tyr Thr Thr Asp Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly
260     265     270
Leu Trp Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
275     280     285
Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
290     295     300
Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
305     310     315     320
Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln
325     330     335
Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp
340     345     350
Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
355     360

```

&lt;210&gt; 26

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; H. sapiens

&lt;400&gt; 26

```

atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc ttagctgggt 60
tctgtaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgccca ctacagtggga 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caagggtcagc actactccaa ttgtcacaa tggtccaacc 420
gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480

```

## Seqlist\_12\_20\_06.txt

```

actgtttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
agtgtttccag tgacaacaac ggtctctacc tttgttcctc caatgccttt gccagggcag 660
aaccatgaac cagtagccac ttcaccatct tcacctcagc cagcagaaac ccaccctacg 720
acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780
gatgggaatg acaccgtgac agagtcttca gatggccttt ggaataacaa tcaaactcaa 840
ctgttcctag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900
tgtatttctg tcttggtgct tcttgctctt ttgggtgtca tcattgccaa aaagtatttc 960
ttcaaaaagg aggttcaaca actaagtgtt tcatttagca gccttcaaat taaagctttg 1020
caaatgcag ttgaaaagga agtccaagca gaagacaata tctacattga gaatagtctt 1080
tatgccacgg actaa 1095

```

<210> 27  
 <211> 364  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(364)  
 <223> TIM-1, allele 6

<400> 27

```

Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1      5      10      15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20     25     30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35     40     45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50     55     60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65     70     75     80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85     90     95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100    105    110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Gly Ile Val Pro Pro Lys
115    120    125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130    135    140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Met Thr Thr
145    150    155    160
Thr Val Pro Thr Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165    170    175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180    185    190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val
195    200    205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210    215    220
Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr
225    230    235    240
Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
245    250    255
Ser Tyr Thr Thr Asp Gly Asp Asp Thr Val Thr Glu Ser Ser Asp Gly
260    265    270
Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
275    280    285
Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
290    295    300
Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
305    310    315    320

```

## Seqlist\_12\_20\_06.txt

Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln  
 325 330 335  
 Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp  
 340 345 350  
 Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp  
 355 360

<210> 28  
 <211> 1099  
 <212> DNA  
 <213> H. sapiens

<400> 28  
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc ttagctggtt 60  
 tctgttaaagg ttgggtggaga ggcagggtcca tctgtcacac taccctgccg ctacagtggg 120  
 gctgtcacat caatgtgtctg gaatagaggc tcatgtttctc tattcacatg ccaaaatggc 180  
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360  
 tcattggaga ttgtgccacc caagggtcacg actactccaa ttgtcacaa tggtccaacc 420  
 gtcacgactg ttccaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacc 480  
 gactgttcca acgacaactg ttccaacaac aatgagcatt ccaacgacaa cgactgttcc 540  
 gacgacaatg actgtttcaa cgacaacgag cgttccaacg acaacgagca ttccaacaac 600  
 aacaagtgtt ccagtgcaca caacgggtctc tacctttgtt cctccaatgc ctttgcccag 660  
 gcagaacccat gaaccagtag ccacttcacc atcttcacct cagccagcag aaaccacccc 720  
 tacgacactg cagggagcaa taaggagaga acccaccagc tcaccattgt actcttacac 780  
 aacagatggg gatgacaccg tgacagagtc ttcagatggc ctttggaata acaatcaaac 840  
 tcaactgttc ctagaacata gtctactgac ggccaatacc actaaaggaa tctatgctgg 900  
 agtctgtatt tctgtcttgg tgcttcttgc tcttttgggt gtcattcatt ccaaaaagta 960  
 tttcttcaaa aaggagggtc aacaactaag tgtttcattt agcagccttc aaattaaagc 1020  
 tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080  
 tctttatgcc acggactaa 1099

<210> 29  
 <211> 301  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(301)  
 <223> TIM-3, allele 1

<400> 29  
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln  
 20 25 30  
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
 35 40 45  
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
 50 55 60  
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
 65 70 75 80  
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
 85 90 95  
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
 100 105 110  
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val  
 115 120 125  
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe  
 130 135 140

## Seqlist\_12\_20\_06.txt

```

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145      150      155      160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
      165      170      175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
      180      185      190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
      195      200      205
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
      210      215      220
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225      230      235      240
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
      245      250      255
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
      260      265      270
Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
      275      280      285
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
      290      295      300

```

<210> 30  
 <211> 1116  
 <212> DNA  
 <213> H. sapiens

```

<400> 30
ggagagttaa aactgtgcct aacagaggtg tcctctgact tttcttctgc aagctccatg 60
ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120
tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
gaatgtggca acgtgggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300
tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360
ctagcagaca gtgggatcta ctgctgcccg atccaaatcc caggcataat gaatgatgaa 420
aaatttaacc tgaagttggt catcaaacca gccaaagtca cccctgcacc gactctgcag 480
agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540
acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600
gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
ggcatctaca tcggagcagg gatctgtgct gggctggctc tggctcttat cttcggcgct 720
ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780
ttggccaacc tccctccctc aggattggca aatgcagtag cagagggaaat tcgctcagaa 840
gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900
tgctatgtca gcagcaggca gcaaccctca caaccttgg gttgtcgctt tgcaatgcca 960
tagatccaac caccttattt ttgagcttgg tgttttgtct ttttcagaaa ctatgagctg 1020
tgtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
cagaagataa tgactcacat gggaattgaa ctggga 1116

```

<210> 31  
 <211> 301  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(301)  
 <223> TIM-3, allele 2

```

<400> 31
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
1      5      10      15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
      20      25      30

```

## Seq1ist\_12\_20\_06.txt

```

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
130 135 140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180 185 190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
195 200 205
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
210 215 220
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225 230 235 240
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
245 250 255
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
260 265 270
Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
275 280 285
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
290 295 300

```

<210> 32  
 <211> 1116  
 <212> DNA  
 <213> H. sapiens

```

<400> 32
ggagagttaa aactgtgcct aacagaggtg tcctctgact tttcttctgc aagctccatg 60
ttttcacatc ttccctttga ctgtgtcctg ctgctgtctg tgctactact tacaagggtc 120
tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
gaatgtggca acgtgggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300
tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360
ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420
aaatttaacc tgaagtgggt catcaaacca gccaaagtca cccctgcacc gactcggcag 480
agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540
acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600
gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
ggcatctaca tcggagcagg gatctgtgct gggctggctc tggctcttat cttcggcgct 720
ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780
ttggccaacc tccctccctc aggatgggca aatgcagtag cagaggggaat tcgctcagaa 840
gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900
tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcca 960
tagatccaac caccttattt ttgagcttgg tgttttgtct ttttcagaaa ctatgagctg 1020
gtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatatt 1080
cagaagataa tgactcacat ggaattgaa ctggga 1116

```

<210> 33

## Seqlist\_12\_20\_06.txt

<211> 378  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(378)  
 <223> TIM-4, allele 1

<400> 33

```

Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1      5      10      15
Leu Tyr Leu Thr Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 20      25      30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 35      40      45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 50      55      60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
 65      70      75      80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
 85      90      95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
 100     105     110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
 115     120     125
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
 130     135     140
Thr Thr Arg Arg Thr Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met
 145     150     155     160
Thr Thr Thr Pro Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
 165     170     175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
 180     185     190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
 195     200     205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
 210     215     220
Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Ala
 225     230     235     240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
 245     250     255
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
 260     265     270
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
 275     280     285
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
 290     295     300
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
 305     310     315     320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
 325     330     335
Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu
 340     345     350
Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly
 355     360     365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu
 370     375

```

<210> 34  
 <211> 1156  
 <212> DNA

&lt;213&gt; H. sapiens

&lt;400&gt; 34

```

atgtccaaag aacctctcat tctctggctg atgattgagt tttgggtggct ttacctgaca 60
ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac tttgccctgt 120
ctgtactcat cctggcttca caacagcaac agcatgtgct gggggaaaga ccagtgcgcc 180
tactccggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcaagaaag 240
tcagcaaaat atagacttca ggggactatc ccgagagggtg atgtctcctt gaccatctta 300
aaccccgatg aaagtgtacag cgggtgtgtac tgctgccgca tagaagtgcc tggctgggtc 360
aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cacgcacaga 420
acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480
acaacaaccc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540
acaccactcc agatgacaac cattgccgtc ttcacaacag caaacacgtg cctttcacta 600
acccaagca cccttccgga ggaagccaca ggtcttctga ctcccagacc ttctaaggaa 660
gggcccattc tcactgcaga atcagaaact gtcctcccca gtgattcctg gagtagtgct 720
gagtctactt ctgctgacac tgtcctgctg acatccaaag agtccaaagt ttgggatctc 780
ccatcaacat cccacgtgtc aatgtggaaa acgagtgatt ctgtgtcttc tcctcagcct 840
ggagcatctg atacagcagt tcctgagcag aacaaaacaa caaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgat gatcatcgcc 960
ccctccttgg gatttgtgct cttcgcatgg tttgtggcgt ttctcctgag agggaaactc 1020
atggaaacct attgttcgca gaaacacaca aggctagact acattggaga tagtaaaaat 1080
gtcctcaatg acgtgcagca tggaaggga gacgaagacg gcctttttac cctctaacaa 1140
cgcagtagca tgtag 1156

```

&lt;210&gt; 35

&lt;211&gt; 378

&lt;212&gt; PRT

&lt;213&gt; H. sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(378)

&lt;223&gt; TIM-4, allele 2

&lt;400&gt; 35

```

Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
1      5      10      15
Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
20     25     30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
35     40     45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
50     55     60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
65     70     75     80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
85     90     95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
100    105    110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
115    120    125
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
130    135    140
Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met
145    150    155    160
Thr Thr Thr Pro Ala Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
165    170    175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
180    185    190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
195    200    205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
210    215    220

```

## Seqlist\_12\_20\_06.txt

```

Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Val
225      230      235      240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
      245      250      255
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
      260      265      270
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
      275      280      285
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
      290      295      300
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
305      310      315      320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
      325      330      335
Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu
      340      345      350
Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly
      355      360      365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu
370      375

```

<210> 36  
 <211> 1156  
 <212> DNA  
 <213> H. sapiens

```

<400> 36
atgtccaaag aacctctcat tctctggctg atgattgagt tttggtggct ttacctgaca 60
ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac tttgccctgt 120
ctgtactcat cctgggtctca caacagcaac agcatgtgct gggggaaaga ccagtgtccc 180
tactccggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcaagaaag 240
tcagcaaaat atagacttca ggggactatc ccgagagggt atgtctcctt gaccatctta 300
aaccacagtg aaagtgcagc cgggtgtgtac tgctgccgca tagaagtgcc tggctgggtc 360
aacgatgtaa agataaacgt ggcctgaat ctacagagag cctcaacaac caccgacaga 420
acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480
acaacaacc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540
acaccactcc agatgacaac cattgccgtc ttcacaacag caaacacgtg cctttcacta 600
accccaagca cccttcaggga ggaagccaca ggtcttctga ctcccgagcc ttctaaggaa 660
gggcccattc tctctgcaga atcagaaact gtcctcccca gtgattcctg gagtagtggt 720
gagtcacttt ctgctgacac tgtcctgctg acatccaaag agtccaaagt ttgggatctc 780
ccatcaacat cccacgtgtc aatgtggaaa acgagtgtt ctgtgtcttc tcctcagcct 840
ggagcatctg atacagcagt tcctgagcag aacaaaacaa caaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgat gatcatcgcc 960
ccctccttgg gatttgtgct cttcgcattg tttgtggcgt ttctcctgag agggaaactc 1020
atggaaacct attgttcgca gaaacacaca aggctagact acattggaga tagtaaaaat 1080
gtcctcaatg acgtgcagca tgggaaggga gacgaagacg gcctttttac cctctaacaa 1140
cgcagtagca tgtagg 1156

```

<210> 37  
 <211> 481  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> exon  
 <222> (152)...(430)  
 <223> Exon 3, reference sequence

```

<400> 37
ttctagctgg gcaatgacca agattgacag ttccaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaagtca cgactactcc aattgtcaca 180

```



## Seqlist\_12\_20\_06.txt

```

actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactggt 240
ccaacgacaa ctgttccaac aacaatgagc attccaacga caacgactgt tctgacgaca 300
atgactgttt caacgacaa gagcgtttcca acgacaacga gcattccaac aacaacaagt 360
gttccagtga caacaactgt ctctaccttt gttcctccaa tgcctttgcc caggcagaac 420
catgaaccag gtaaaacaga tgtgtttgga agcccaaagg ccttctaata aggagctgcg 480
g 481

```

<210> 38  
 <211> 499  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> exon  
 <222> (152)...(448)  
 <223> Exon 3, INS157 polymorphism

```

<400> 38
ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaagtca cgactactcc aattgtcaca 180
actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactggt 240
ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
attccaacaa caacaagtgt tccagtgaac acaactgtct ctacctttgt tccccaatg 420
cctttgccca ggcagaacca tgaaccaggt aaaacagatg tgtttggaag cccaaaggcc 480
ttctaatagag gagctgcgg 499

```

<210> 39  
 <211> 496  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> exon  
 <222> (152)...(445)  
 <223> Exon 3, 195delT polymorphism

```

<400> 39
ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaagtca cgactactcc aattgtcaca 180
actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactggt 240
ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
attccaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
ttgccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480
taatgaggag ctgcgg 496

```

<210> 40  
 <211> 496  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> exon  
 <222> (152)...(445)  
 <223> Exon 3, 157insMTTVP polymorphism

```

<400> 40
ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaagtca cgactactcc aattgtcaca 180

```

## Seqlist\_12\_20\_06.txt

actgttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactgtt 240  
 ccaatgacga ctgttccaac gacaactgtt ccaacaacaa tgagcattcc aacgacaacg 300  
 actgttctga cgacaatgac tgtttcaacg acaacgagcg ttccaacgac aacgagcatt 360  
 ccaacaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420  
 ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480  
 taatgaggag ctgcgg 496

<210> 41  
 <211> 18  
 <212> DNA  
 <213> H. sapiens

<400> 41  
 gtgtctgaca gtggcgta 18

<210> 42  
 <211> 18  
 <212> DNA  
 <213> H. sapiens

<400> 42  
 ttgcccagg cagaacca 18

<210> 43  
 <211> 18  
 <212> DNA  
 <213> H. sapiens

<400> 43  
 ccaccaagg tcacgact 18

<210> 44  
 <211> 18  
 <212> DNA  
 <213> H. sapiens

<400> 44  
 atgccacgga ctaagacc 18

<210> 45  
 <211> 41  
 <212> DNA  
 <213> H. sapiens

<400> 45  
 ggaattcgtc gaccaccatg catcctcaag tggatcatctt a 41

<210> 46  
 <211> 42  
 <212> DNA  
 <213> H. sapiens

<400> 46  
 ggaattcgcg gccgctcatt agtccgtggc ataaacagta tt 42

<210> 47  
 <211> 20  
 <212> DNA  
 <213> H. sapiens

<400> 47  
 tcaagtggtc atcttaagcc 20

seqlist\_12\_20\_06.txt

```

<210> 48
<211> 22
<212> DNA
<213> H. sapiens

<400> 48
taaactctca aagagcacca ct                22

<210> 49
<211> 22
<212> DNA
<213> H. sapiens

<400> 49
acagactcca gcatagattc ct                22

<210> 50
<211> 22
<212> DNA
<213> H. sapiens

<400> 50
gcaccaagac agaaatacag ac                22

<210> 51
<211> 31
<212> DNA
<213> H. sapiens

<400> 51
agaagcaccc aagacagaaa tacagactcc a      31

<210> 52
<211> 19
<212> DNA
<213> H. sapiens

<400> 52
ttctagctgg gcaatgacc                    19

<210> 53
<211> 20
<212> DNA
<213> H. sapiens

<400> 53
ccgcagctcc tcattagaag                    20

<210> 54
<211> 307
<212> PRT
<213> rattus norvegicus

<400> 54
Met Val Gln Leu Gln Val Phe Ile Ser Gly Leu Leu Leu Leu Leu Pro
 1         5         10        15
Gly Ser Val Asp Ser Tyr Glu Val Val Lys Gly Val Val Gly His Pro
 20        25        30
Val Thr Ile Pro Cys Thr Tyr Ser Thr Arg Gly Gly Ile Thr Thr Thr
 35        40        45
Cys Trp Gly Arg Gly Gln Cys Pro Tyr Ser Ser Cys Gln Asn Ile Leu

```

## Seq1ist\_12\_20\_06.txt

```

50      55      60
Ile Trp Thr Asn Gly Tyr Gln Val Thr Tyr Arg Ser Ser Gly Arg Tyr
65      70      75      80
Asn Ile Lys Gly Arg Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
85      90      95
Asn Ser Val Asp Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
100     105     110
Pro Gly Trp Phe Asn Asp Gln Lys Met Thr Phe Ser Leu Glu Val Lys
115     120     125
Pro Glu Ile Pro Thr Ser Pro Pro Thr Arg Pro Thr Thr Thr Arg Pro
130     135     140
Thr Thr Thr Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro
145     150     155     160
Thr Ser Thr Arg Val Ser Thr Ser Thr Pro Thr Pro Glu Gln Thr Gln
165     170     175
Thr His Lys Pro Glu Ile Thr Thr Phe Tyr Ala His Glu Thr Thr Ala
180     185     190
Glu Val Thr Glu Thr Pro Ser Tyr Thr Pro Ala Asp Trp Asn Gly Thr
195     200     205
Val Thr Ser Ser Glu Glu Ala Trp Asn Asn His Thr Val Arg Ile Pro
210     215     220
Leu Arg Lys Pro Gln Arg Asn Pro Thr Lys Gly Phe Tyr Val Gly Met
225     230     235     240
Ser Val Ala Ala Leu Leu Leu Leu Leu Ala Ser Thr Val Val Val
245     250     255
Thr Arg Tyr Ile Ile Ile Arg Lys Lys Met Gly Ser Leu Ser Phe Val
260     265     270
Ala Phe His Val Ser Lys Ser Arg Ala Leu Gln Asn Ala Ala Ile Val
275     280     285
His Pro Arg Ala Glu Asp Asn Ile Tyr Ile Ile Glu Asp Arg Ser Arg
290     295     300
Gly Ala Glu
305

```

&lt;210&gt; 55

&lt;211&gt; 451

&lt;212&gt; PRT

&lt;213&gt; Chlorocebus aethiops

&lt;400&gt; 55

```

Met His Leu Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1      5      10      15
Ser Val Ala Asp Ser Val Asn Val Asp Gly Val Ala Gly Leu Ser Ile
20      25      30
Thr Leu Pro Cys Arg Tyr Asn Gly Ala Ile Thr Ser Met Cys Trp Asn
35      40      45
Arg Gly Thr Cys Ser Val Phe Ser Cys Pro Asp Gly Ile Val Trp Thr
50      55      60
Asn Gly Thr His Val Thr Tyr Arg Lys Glu Thr Arg Tyr Lys Leu Leu
65      70      75      80
Gly Asn Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Ala Asn Thr Ala
85      90      95
Val Ser Asp Ser Gly Ile Tyr Cys Cys Arg Val Lys His Ser Gly Trp
100     105     110
Phe Asn Asp Met Lys Ile Thr Ile Ser Leu Lys Ile Gly Pro Pro Arg
115     120     125
Val Thr Thr Pro Ile Val Arg Thr Val Arg Thr Ser Thr Thr Val Pro
130     135     140
Thr Thr Thr Thr Leu Pro Thr Thr Thr Thr Leu Pro Thr Thr Thr
145     150     155     160
Leu Pro Thr Thr Thr Leu Pro Met Thr Thr Thr Leu Pro Met Thr
165     170     175
Thr Thr Leu Pro Thr Thr Thr Thr Val Pro Thr Thr Thr Thr Leu Pro

```

[illegible]

```
<210> 56
<211> 359
<212> PRT
<213> H. sapiens
```

<400>	56															
Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp	
1				5					10					15		
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val	
			20					25					30			
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn	
		35					40					45				
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr	
	50					55					60					
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu	
65					70					75					80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala	
				85					90					95		
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp	
			100					105					110			
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys	
		115					120					125				
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val	
	130					135					140					
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr	
145					150					155					160	

## Seq1ist\_12\_20\_06.txt

Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr  
 165 170 175  
 Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro  
 180 185 190  
 Thr Thr Thr Ser Val Pro Val Thr Thr Thr Val Ser Thr Phe Val Pro  
 195 200 205  
 Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro  
 210 215 220  
 Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala  
 225 230 235 240  
 Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp  
 245 250 255  
 Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn  
 260 265 270  
 Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr  
 275 280 285  
 Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala  
 290 295 300  
 Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val  
 305 310 315 320  
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln  
 325 330 335  
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu  
 340 345 350  
 Asn Ser Leu Tyr Ala Thr Asp  
 355

<210> 57  
 <211> 6  
 <212> PRT  
 <213> H. sapiens

<400> 57  
 Met Thr Thr Thr Val Pro  
 1 5

<210> 58  
 <211> 7  
 <212> PRT  
 <213> H. sapiens

<400> 58  
 Ser Val Val Tyr Gly Leu Arg  
 1 5